

<110> Kaneka Corporation

<120> NOVEL CARBONYL REDUCTASE, GENE THEREFOR, AND METHOD OF USING THE SAME

<130> T609HOP-GT

<150> JP2000-232756

<151> 2000-08-01

<160> 11

<210> 1

<211> 277

<212> PRT

<213> Micrococcus luteus

<400> 1

Met Arg Arg Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly

1 5 10 15

Gln Gly Thr Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu

20 25 30

Val Ala Ala Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp

35 40 45

Thr Ala Glu Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu

50 55 60

Ala Leu Ala Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met

65 70 75 80

Pro Ser His Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser

85 90 95

Leu Lys Arg Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp

	100		105		110
Gln Gly Arg Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu					
115		120		125	
Val Glu Asp Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Phe Asp His					
130		135		140	
Arg Ala Leu Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr					
145		150		155	160
Thr Asp Gln Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp					
	165		170		175
Leu Leu Pro Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser					
	180		185		190
Pro Ile Glu Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val					
195		200		205	
Ala Ala Arg His Ser Val Ser Pro Ala Ala Ala Ala Leu Ala Trp Val					
210		215		220	
Leu Arg Arg Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln					
225		230		235	240
His Val Arg Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu					
	245		250		255
Asp Leu Asp Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg					
	260		265		270
Pro Leu Glu Met Leu					
275					

 $\langle 210 \rangle$ 2

<211> 834

<212> DNA

<213> Micrococcus luteus

<400> 2

atg cga cgg atg acg ctg ccg agt ggg gag tcc atc cct gtg ctg ggc
 Met Arg Arg Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly
 1 5 10 15

cag ggc acc tgg ggc tgg ggt gag gac ccc ggc cgc cgc ggc gac gag
 Gln Gly Thr Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu
 20 25 30

gtc gcc gcg ctg cac gcc ggc ctc gag ctg ggc atg acg ctg gtc gac
 Val Ala Ala Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp
 35 40 45

acc gcc gag atg tac gcc gac ggc ggt gcg gag gag gtg gct ggt gaa
 Thr Ala Glu Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu
 50 55 60

gca ttg gcg ggt cgc cgc gac gag gcg ttc gtg gtc agc aag gtc atg
 Ala Leu Ala Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met
 65 70 75 80

ccg tcc cac gcc tcc cgt tcc ggc acg atc gcg gcc tgc gaa cgc agc
 Pro Ser His Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser
 85 90 95

ctg aaa cgc ctg ggc acc gat cgg atc gac ctc tac ctg ctg cac tgg
 Leu Lys Arg Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp
 100 105 110

cag ggc agg tac ccg ctg cag gac acc gtc gcg gcc ttc cac cag ctc
 Gln Gly Arg Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu
 115 120 125

gtc gag gac ggg aaa atc cga tac tgg ggc gtc agc aac ttc gac cac
 Val Glu Asp Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Phe Asp His
 130 135 140

cgg gcc ctc gcc gag ctg cag gac gtg ccg ggc acc agc ggg ctg acc
 Arg Ala Leu Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr
 145 150 155 160

acg gat cag gtg ctg tac aac ctg tcg ccg cga gga ccg gag tac gac
 Thr Asp Gln Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp
 165 170 175

ctg ctg ccg tgg tgc gcc gac cac cag ctg ccg gtc atg gcg tac tcg
 Leu Leu Pro Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser
 180 185 190

ccg atc gag cag ggc cgc atc ctt gac gac acg acg ctg aac gac gtc
 Pro Ile Glu Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val
 195 200 205

gcg gcc cgt cac agc gtc agc ccc gcg gcg gcg gcc ctt gcc tgg gtg
 Ala Ala Arg His Ser Val Ser Pro Ala Ala Ala Leu Ala Trp Val
 210 215 220

ctg cgc cgc gac tcg ctc tgc acg atc ccc aag gcg agc agc ccg cag
 Leu Arg Arg Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln
 225 230 235 240

cac gtg cgc gac aac gcc aca gca ctg gac gtg gag ctg acc cgc gaa
 His Val Arg Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu
 245 250 255

gac ctg gat gct ctg gac cgt gcg ttt ccg ccc ccg agc gga ccg cga
 Asp Leu Asp Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg
 260 265 270

cca ctg gaa atg ctg tga
 Pro Leu Glu Met Leu
 275

$\langle 220 \rangle$

<400> 6

32

<213> Artificial Sequence

46

<213> Artificial Sequence

29

<213> Artificial Sequence

60

gttttaggtc aaggtacttg gggttggggg gaagatccag gtcgtcgtgg tgatgaagtt 120

gctgctttac atgctggtct cgag

<210> 10

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 10

caggagctct aaggaggta acaatgtata aag

33

<210> 11

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 11

cacggatctt tatccgcgtc ctgcttgg

28

